Victor L Davidson

List of Publications by Year
in descending order

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204 papers	5,974 citations	50276 46 h-index	106344 65 g-index
239 all docs	239 docs citations	239 times ranked	2532 citing authors

#	Article	IF	Citations
1	The hemerythrin-like diiron protein from Mycobacterium kansasii is a nitric oxide peroxidase. Journal of Biological Chemistry, 2022, , 101696.	3.4	2
2	Substitution of the sole tryptophan of the cupredoxin, amicyanin, with 5-hydroxytryptophan alters fluorescence properties and energy transfer to the type 1 copper site. Journal of Inorganic Biochemistry, 2022, 234, 111895.	3.5	2
3	Diversity of structures and functions of oxo-bridged non-heme diiron proteins. Archives of Biochemistry and Biophysics, 2021, 705, 108917.	3.0	14
4	Protein-Derived Cofactors. , 2020, , 40-57.		2
5	Correlation of Conservation of Sequence and Structures of Mycobacterial Hemerythrin-like Proteins with Evolutionary Relationship and Host Pathogenicity. ACS Omega, 2020, 5, 23385-23392.	3.5	2
6	Crystal structure of a hemerythrin-like protein from Mycobacterium kansasii and homology model of the orthologous Rv2633c protein of M. tuberculosis. Biochemical Journal, 2020, 477, 567-581.	3.7	8
7	Roles of active-site residues in catalysis, substrate binding, cooperativity, and the reaction mechanism of the quinoprotein glycine oxidase. Journal of Biological Chemistry, 2020, 295, 6472-6481.	3.4	2
8	The Redox Properties of a Cysteine Tryptophylquinone-Dependent Glycine Oxidase Are Distinct from Those of Tryptophylquinone-Dependent Dehydrogenases. Biochemistry, 2019, 58, 2243-2249.	2.5	3
9	Characterization of PlGoxB, a flavoprotein required for cysteine tryptophylquinone biosynthesis in glycine oxidase from Pseudoalteromonas luteoviolacea. Archives of Biochemistry and Biophysics, 2019, 674, 108110.	3.0	3
10	Kinetic and structural evidence that Asp-678 plays multiple roles in catalysis by the quinoprotein glycine oxidase. Journal of Biological Chemistry, 2019, 294, 17463-17470.	3.4	2
11	Structural and Spectroscopic Characterization of a Product Schiff Base Intermediate in the Reaction of the Quinoprotein Glycine Oxidase, GoxA. Biochemistry, 2019, 58, 706-713.	2.5	4
12	Protein-Derived Cofactors Revisited: Empowering Amino Acid Residues with New Functions. Biochemistry, 2018, 57, 3115-3125.	2.5	28
13	Structure and Enzymatic Properties of an Unusual Cysteine Tryptophylquinone-Dependent Glycine Oxidase from Pseudoalteromonas luteoviolacea. Biochemistry, 2018, 57, 1155-1165.	2.5	18
14	Metabolomics reveals critical adrenergic regulatory checkpoints in glycolysis and pentoseâ€“phosphate pathways in embryonic heart. Journal of Biological Chemistry, 2018, 293, 6925-6941.	3.4	13
15	The Rv2633c protein of Mycobacterium tuberculosis is a non-heme di-iron catalase with a possible role in defenses against oxidative stress. Journal of Biological Chemistry, 2018, 293, 1590-1595.	3.4	19
16	Diversity of structures, catalytic mechanisms and processes of cofactor biosynthesis of tryptophylquinone-bearing enzymes. Archives of Biochemistry and Biophysics, 2018, 654, 40-46.	3.0	10
17	Quinone Cofactors. , 2018, , 1-4.		0
18	Coupled Electron Transfer. , 2018, , 1-3.		0

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19	Electron Transfer Theory. , 2018, , 1-5.		0
20	Roles of Copper and a Conserved Aspartic Acid in the Autocatalytic Hydroxylation of a Specific Tryptophan Residue during Cysteine Tryptophylquinone Biogenesis. Biochemistry, 2017, 56, 997-1004.	2.5	7
21	Properties of the highâ€spin heme of MauG are altered by binding of preMADH at the protein surface 40 Ã… away. FEBS Letters, 2017, 591, 1566-1572.	2.8	1
22	Ascorbate protects the diheme enzyme, MauG, against self-inflicted oxidative damage by an unusual antioxidant mechanism. Biochemical Journal, 2017, 474, 2563-2572.	3.7	2
23	Analytical Methods for Assessing the Effects of Site-Directed Mutagenesis on Proteinâ€“Cofactor and Proteinâ€“Protein Functional Relationships. Methods in Molecular Biology, 2017, 1498, 421-438.	0.9	1
24	In Silico Approaches to Identify Mutagenesis Targets to Probe and Alter Proteinâ€“Cofactor and Proteinâ€“Protein Functional Relationships. Methods in Molecular Biology, 2017, 1498, 181-190.	0.9	2
25	Interaction of GoxA with Its Modifying Enzyme and Its Subunit Assembly Are Dependent on the Extent of Cysteine Tryptophylquinone Biosynthesis. Biochemistry, 2016, 55, 2305-2308.	2.5	10
26	MauG, a Diheme Enzyme Involved in the Synthesis of the Enzyme Cofactor, Tryptophan Tryptophylquinone. , 2016, , 1-30.		8
27	Mechanism of protein oxidative damage that is coupled to long-range electron transfer to high-valent haems. Biochemical Journal, 2016, 473, 1769-1775.	3.7	14
28	A Suicide Mutation Affecting Proton Transfers to High-Valent Hemes Causes Inactivation of MauG during Catalysis. Biochemistry, 2016, 55, 5738-5745.	2.5	6
29	Roles of Conserved Residues of the Glycine Oxidase GoxA in Controlling Activity, Cooperativity, Subunit Composition, and Cysteine Tryptophylquinone Biosynthesis. Journal of Biological Chemistry, 2016, 291, 23199-23207.	3.4	13
30	Acoustic Injectors for Drop-On-Demand Serial Femtosecond Crystallography. Structure, 2016, 24, 631-640.	3.3	88
31	Converting the bis-FeIV state of the diheme enzyme MauG to Compound I decreases the reorganization energy for electron transfer. Biochemical Journal, 2016, 473, 67-72.	3.7	1
32	Use of the amicyanin signal sequence for efficient periplasmic expression in E. coli of a human antibody light chain variable domain. Protein Expression and Purification, 2015, 108, 9-12.	1.3	11
33	A T67A mutation in the proximal pocket of the high-spin heme of MauG stabilizes formation of a mixed-valent FeII/FeIII state and enhances charge resonance stabilization of the bis-FeIV state. Biochimica Et Biophysica Acta - Bioenergetics, 2015, 1847, 709-716.	1.0	4
34	Roles of active site residues in LodA, a cysteine tryptophylquinone dependent Îµ-lysine oxidase. Archives of Biochemistry and Biophysics, 2015, 579, 26-32.	3.0	17
35	Characterization of the free energy dependence of an interprotein electron transfer reaction by variation of pH and site-directed mutagenesis. Biochimica Et Biophysica Acta - Bioenergetics, 2015, 1847, 1181-1186.	1.0	2
36	Roles of multiple-proton transfer pathways and proton-coupled electron transfer in the reactivity of the bis-FeIV state of MauG. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10896-10901.	7.1	19

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37	Characterization of recombinant biosynthetic precursors of the cysteine tryptophylquinone cofactors of l-lysine-epsilon-oxidase and glycine oxidase from Marinomonas mediterranea. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1123-1131.	2.3	20
38	Mechanisms for control of biological electron transfer reactions. Bioorganic Chemistry, 2014, 57, 213-221.	4.1	20
39	Steadyâ€state kinetic mechanism of LodA, a novel cysteine tryptophylquinoneâ€dependent oxidase. FEBS Letters, 2014, 588, 752-756.	2.8	12
40	MauG, a diheme enzyme that catalyzes tryptophan tryptophylquinone biosynthesis by remote catalysis. Archives of Biochemistry and Biophysics, 2014, 544, 112-118.	3.0	6
41	Site-Directed Mutagenesis of Gln103 Reveals the Influence of This Residue on the Redox Properties and Stability of MauG. Biochemistry, 2014, 53, 1342-1349.	2.5	10
42	The sole tryptophan of amicyanin enhances its thermal stability but does not influence the electronic properties of the type 1 copper site. Archives of Biochemistry and Biophysics, 2014, 550-551, 20-27.	3.0	7
43	A simple method to engineer a protein-derived redox cofactor for catalysis. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 1595-1601.	1.0	2
44	Oxidative Damage in MauG: Implications for the Control of High-Valent Iron Species and Radical Propagation Pathways. Biochemistry, 2013, 52, 9447-9455.	2.5	25
45	Diradical intermediate within the context of tryptophan tryptophylquinone biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4569-4573.	7.1	51
46	A Trp199Glu MauG variant reveals a role for Trp199 interactions with preâ€methylamine dehydrogenase during tryptophan tryptophylquinone biosynthesis. FEBS Letters, 2013, 587, 1736-1741.	2.8	3
47	Gated Electron Transfer. , 2013, , 886-888.		0
48	Quinone Cofactors. , 2013, , 2166-2168.		1
49	Posttranslational Biosynthesis of the Protein-Derived Cofactor Tryptophan Tryptophylquinone. Annual Review of Biochemistry, 2013, 82, 531-550.	11.1	36
50	Carboxyl Group of Glu113 Is Required for Stabilization of the Diferrous and Bis-Fe^{IV} States of MauG. Biochemistry, 2013, 52, 6358-6367.	2.5	14
51	Mutation of Trp93 of MauG to tyrosine causes loss of bound Ca2+ and alters the kinetic mechanism of tryptophan tryptophylquinone cofactor biosynthesis. Biochemical Journal, 2013, 456, 129-137.	3.7	7
52	Structures of MauG in complex with quinol and quinone MADH. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 738-743.	0.7	5
53	Tryptophan-mediated charge-resonance stabilization in the bis -Fe(IV) redox state of MauG. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 9639-9644.	7.1	63
54	Effects of the loss of the axial tyrosine ligand of the lowâ€spin heme of MauG on its physical properties and reactivity. FEBS Letters, 2012, 586, 4339-4343.	2.8	16

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55	Proline 107 Is a Major Determinant in Maintaining the Structure of the Distal Pocket and Reactivity of the High-Spin Heme of MauG. Biochemistry, 2012, 51, 1598-1606.	2.5	30
56	Role of Calcium in Metalloenzymes: Effects of Calcium Removal on the Axial Ligation Geometry and Magnetic Properties of the Catalytic Diheme Center in MauG. Biochemistry, 2012, 51, 1586-1597.	2.5	30
57	Tryptophan tryptophylquinone biosynthesis: A radical approach to posttranslational modification. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 1299-1305.	2.3	13
58	Geometric and electronic structures of the Hisâ€“Fe(IV)=O and Hisâ€“Fe(IV)â€“Tyr hemes of MauG. Journal of Biological Inorganic Chemistry, 2012, 17, 1241-1255.	2.6	20
59	Characterization of Electron Tunneling and Hole Hopping Reactions between Different Forms of MauG and Methylamine Dehydrogenase within a Natural Protein Complex. Biochemistry, 2012, 51, 6942-6949.	2.5	39
60	Generation of protein-derived redoxcofactors by posttranslational modification. Molecular BioSystems, 2011, 7, 29-37.	2.9	43
61	Crystal Structures of CO and NO Adducts of MauG in Complex with Pre-Methylamine Dehydrogenase: Implications for the Mechanism of Dioxygen Activation. Biochemistry, 2011, 50, 2931-2938.	2.5	20
62	Proline 96 of the Copper Ligand Loop of Amicyanin Regulates Electron Transfer from Methylamine Dehydrogenase by Positioning Other Residues at the Proteinâ^'Protein Interface. Biochemistry, 2011, 50, 1265-1273.	2.5	7
63	The Tightly Bound Calcium of MauG Is Required for Tryptophan Tryptophylquinone Cofactor Biosynthesis. Biochemistry, 2011, 50, 144-150.	2.5	17
64	Cupredoxinsâ€"A study of how proteins may evolve to use metals for bioenergetic processes. Metallomics, 2011, 3, 140.	2.4	76
65	Mutagenesis of tryptophan199 suggests that hopping is required for MauG-dependent tryptophan tryptophylquinone biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 16956-16961.	7.1	65
66	Replacement of the axial copper ligand methionine with lysine in amicyanin converts it to a zinc-binding protein that no longer binds copper. Journal of Inorganic Biochemistry, 2011, 105, 1638-1644.	3.5	4
67	The many faces of a proton. Nature Chemistry, 2011, 3, 662-663.	13.6	14
68	Protein-Derived Cofactors. , 2010, , 675-710.		3
69	In Crystallo Posttranslational Modification Within a MauG/Preâ€“Methylamine Dehydrogenase Complex. Science, 2010, 327, 1392-1394.	12.6	117
70	Unprecedented Fe(IV) Species in a Diheme Protein MauG: A Quantum Chemical Investigation on the Unusual MÃ¶ssbauer Spectroscopic Properties. Journal of Physical Chemistry Letters, 2010, 1, 2936-2939.	4.6	30
71	Long-Range Electron Transfer Reactions between Hemes of MauG and Different Forms of Tryptophan Tryptophylquinone of Methylamine Dehydrogenase. Biochemistry, 2010, 49, 5810-5816.	2.5	25
72	Functional Importance of Tyrosine 294 and the Catalytic Selectivity for the Bis-Fe(IV) State of MauG Revealed by Replacement of This Axial Heme Ligand with Histidine,. Biochemistry, 2010, 49, 9783-9791.	2.5	42

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73	Uncovering novel biochemistry in the mechanism of tryptophan tryptophylquinone cofactor biosynthesis. Current Opinion in Chemical Biology, 2009, 13, 469-474.	6.1	29
74	Kinetic Mechanism for the Initial Steps in MauG-Dependent Tryptophan Tryptophylquinone Biosynthesis. Biochemistry, 2009, 48, 2442-2447.	2.5	47
75	Suicide Inactivation of MauG during Reaction with O₂ or H₂O₂ in the Absence of Its Natural Protein Substrate. Biochemistry, 2009, 48, 10106-10112.	2.5	20
76	Defining the Role of the Axial Ligand of the Type 1 Copper Site in Amicyanin by Replacement of Methionine with Leucine. Biochemistry, 2009, 48, 9174-9184.	2.5	17
77	Heme Iron Nitrosyl Complex of MauG Reveals an Efficient Redox Equilibrium between Hemes with Only One Heme Exclusively Binding Exogenous Ligands. Biochemistry, 2009, 48, 11603-11605.	2.5	21
78	The axial ligand and extent of protein folding determine whether Zn or Cu binds to amicyanin. Journal of Inorganic Biochemistry, 2008, 102, 342-346.	3.5	7
79	Protein Control of True, Gated, and Coupled Electron Transfer Reactions. Accounts of Chemical Research, 2008, 41, 730-738.	15.6	102
80	Kinetic and Physical Evidence That the Diheme Enzyme MauG Tightly Binds to a Biosynthetic Precursor of Methylamine Dehydrogenase with Incompletely Formed Tryptophan Tryptophylquinone. Biochemistry, 2008, 47, 2908-2912.	2.5	21
81	A catalytic di-heme bis -Fe(IV) intermediate, alternative to an Fe(IV)=O porphyrin radical. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8597-8600.	7.1	89
82	Detection of Transient Intermediates in the Metal-Dependent Nonoxidative Decarboxylation Catalyzed by Î±-Amino-Î²-Carboxymuconate-Îµ-Semialdehyde Decarboxylase. Journal of the American Chemical Society, 2007, 129, 9278-9279.	13.7	20
83	Correlation of Rhombic Distortion of the Type 1 Copper Site of M98Q Amicyanin with Increased Electron Transfer Reorganization Energy. Biochemistry, 2007, 46, 8561-8568.	2.5	9
84	Protein-Derived Cofactors. Expanding the Scope of Post-Translational Modifications. Biochemistry, 2007, 46, 5283-5292.	2.5	69
85	Generation of Novel Copper Sites by Mutation of the Axial Ligand of Amicyanin. Atomic Resolution Structures and Spectroscopic Properties,. Biochemistry, 2007, 46, 1900-1912.	2.5	21
86	A Single Methionine Residue Dictates the Kinetic Mechanism of Interprotein Electron Transfer from Methylamine Dehydrogenase to Amicyanin[,]. Biochemistry, 2007, 46, 11137-11146.	2.5	13
87	Tracking X-ray-derived redox changes in crystals of a methylamine dehydrogenase/amicyanin complex using single-crystal UV/Vis microspectrophotometry. Journal of Synchrotron Radiation, 2007, 14, 92-98.	2.4	37
88	Crystal Structure of an Electron Transfer Complex between Aromatic Amine Dehydrogenase and Azurin from Alcaligenes faecalis,. Biochemistry, 2006, 45, 13500-13510.	2.5	34
89	Evidence for Redox Cooperativity betweenc-Type Hemes of MauG Which Is Likely Coupled to Oxygen Activation during Tryptophan Tryptophylquinone Biosynthesisâ€. Biochemistry, 2006, 45, 821-828.	2.5	59
90	Mechanistic Possibilities in MauG-Dependent Tryptophan Tryptophylquinone Biosynthesisâ€. Biochemistry, 2006, 45, 13276-13283.	2.5	45

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91	Site-Directed Mutagenesis of Proline 52 To Glycine in Amicyanin Converts a True Electron Transfer Reaction into One that Is Conformationally Gated,. Biochemistry, 2006, 45, 8284-8293.	2.5	15
92	Isotope Labeling Studies Reveal the Order of Oxygen Incorporation into the Tryptophan Tryptophylquinone Cofactor of Methylamine Dehydrogenase. Journal of the American Chemical Society, 2006, 128, 12416-12417.	13.7	23
93	Involvement of a Putative [Fe-S]-cluster-binding Protein in the Biogenesis of Quinohemoprotein Amine Dehydrogenase. Journal of Biological Chemistry, 2006, 281, 13672-13684.	3.4	30
94	Structure and mechanism of tryptophylquinone enzymes. Bioorganic Chemistry, 2005, 33, 159-170.	4.1	20
95	Active Site Aspartate Residues Are Critical for Tryptophan Tryptophylquinone Biogenesis in Methylamine Dehydrogenase. Journal of Biological Chemistry, 2005, 280, 17392-17396.	3.4	15
96	Site-Directed Mutagenesis of Proline 94 to Alanine in Amicyanin Converts a True Electron Transfer Reaction into One That Is Kinetically Coupledâ€. Biochemistry, 2005, 44, 7200-7206.	2.5	16
97	MauG-Dependent in Vitro Biosynthesis of Tryptophan Tryptophylquinone in Methylamine Dehydrogenase. Journal of the American Chemical Society, 2005, 127, 8258-8259.	13.7	52
98	The ligand geometry of copper determines the stability of amicyanin. Archives of Biochemistry and Biophysics, 2005, 444, 27-33.	3.0	13
99	Electron transfer in crystals of the binary and ternary complexes of methylamine dehydrogenase with amicyanin and cytochrome c551i as detected by EPR spectroscopy. Journal of Biological Inorganic Chemistry, 2004, 9, 231-237.	2.6	14
100	Crystallographic and NMR Investigation of Cobalt-Substituted Amicyanin,. Biochemistry, 2004, 43, 9381-9389.	2.5	12
101	Further Insights into Quinone Cofactor Biogenesis:Â Probing the Role ofmauGin Methylamine Dehydrogenase Tryptophan Tryptophylquinone Formationâ€. Biochemistry, 2004, 43, 5494-5502.	2.5	76
102	Structural Studies of Two Mutants of Amicyanin from Paracoccus denitrificans That Stabilize the Reduced State of the Copper,. Biochemistry, 2004, 43, 9372-9380.	2.5	37
103	Electron transfer in quinoproteins. Archives of Biochemistry and Biophysics, 2004, 428, 32-40.	3.0	68
104	X-ray structure of methanol dehydrogenase from Paracoccus denitrificans and molecular modeling of its interactions with cytochrome c-551i. Journal of Biological Inorganic Chemistry, 2003, 8, 843-854.	2.6	30
105	Probing mechanisms of catalysis and electron transfer by methylamine dehydrogenase by site-directed mutagenesis of Î±Phe55. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1647, 230-233.	2.3	7
106	Evidence for Substrate Activation of Electron Transfer from Methylamine Dehydrogenase to Amicyanin. Journal of the American Chemical Society, 2003, 125, 3224-3225.	13.7	11
107	MauG, a Novel Diheme Protein Required for Tryptophan Tryptophylquinone Biogenesis. Biochemistry, 2003, 42, 7318-7325.	2.5	123
108	Understanding Quinone Cofactor Biogenesis in Methylamine Dehydrogenase through Novel Cofactor Generationâ€. Biochemistry, 2003, 42, 3224-3230.	2.5	21

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109	Chemical and Kinetic Reaction Mechanisms of Quinohemoprotein Amine Dehydrogenase from Paracoccus denitrificans. Biochemistry, 2003, 42, 10896-10903.	2.5	24
110	Effects of Engineering Uphill Electron Transfer into the Methylamine Dehydrogenaseâ^'Amicyaninâ^'Cytochromec-551i Complexâ€. Biochemistry, 2003, 42, 1772-1776.	2.5	11
111	An Engineered CuA Amicyanin Capable of Intermolecular Electron Transfer Reactions. Journal of Biological Chemistry, 2003, 278, 47269-47274.	3.4	21
112	Use of Indirect Site-directed Mutagenesis to Alter the Substrate Specificity of Methylamine Dehydrogenase. Journal of Biological Chemistry, 2002, 277, 4119-4122.	3.4	11
113	Mechanisms of Catalysis and Electron Transfer by Tryptophan Tryptophylquinone Enzymes. Progress in Reaction Kinetics and Mechanism, 2002, 27, 209-241.	2.1	4
114	Improved Sensitivity of a Histamine Sensor Using an Engineered Methylamine Dehydrogenase. Analytical Chemistry, 2002, 74, 1144-1148.	6.5	48
115	Mutation of Î±Phe55 of Methylamine Dehydrogenase Alters the Reorganization Energy and Electronic Coupling for Its Electron Transfer Reaction with Amicyanin,. Biochemistry, 2002, 41, 13926-13933.	2.5	21
116	Chemically Gated Electron Transfer. A Means of Accelerating and Regulating Rates of Biological Electron Transferâ€. Biochemistry, 2002, 41, 14633-14636.	2.5	48
117	Lysozyme-Osmotic Shock Methods for Localization of Periplasmic Redox Proteins in Bacteria. Methods in Enzymology, 2002, 353, 121-130.	1.0	13
118	Redox properties of an engineered purple CuA azurin. Archives of Biochemistry and Biophysics, 2002, 404, 158-162.	3.0	2
119	Inter-subunit cross-linking of methylamine dehydrogenase by cyclopropylamine requires residue Î±Phe55. FEBS Letters, 2002, 517, 172-174.	2.8	1
120	Re-Engineering Monovalent Cation Binding Sites of Methylamine Dehydrogenase:Â Effects on Spectral Properties and Gated Electron Transferâ€. Biochemistry, 2001, 40, 12285-12291.	2.5	18
121	Pyrroloquinoline quinone (PQQ) from methanol dehydrogenase and tryptophan tryptophylquinone (TTQ) from methylamine dehydrogenase. Advances in Protein Chemistry, 2001, 58, 95-140.	4.4	77
122	Active-site residues are critical for the folding and stability of methylamine dehydrogenase. Protein Engineering, Design and Selection, 2001, 14, 675-681.	2.1	12
123	Reaction products and intermediates of tryptophan tryptophylquinone enzymes. Journal of Molecular Catalysis B: Enzymatic, 2000, 8, 69-83.	1.8	3
124	Methylamine Dehydrogenase Structure and Function of Electron Transfer Complexes. Sub-Cellular Biochemistry, 2000, 35, 119-143.	2.4	6
125	Tyr30 of amicyanin is not critical for electron transfer to cytochrome c-551i: implications for predicting electron transfer pathways. Biochimica Et Biophysica Acta - Bioenergetics, 2000, 1457, 27-35.	1.0	8
126	What Controls the Rates of Interprotein Electron-Transfer Reactions. Accounts of Chemical Research, 2000, 33, 87-93.	15.6	139

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127	Conversion of Methylamine Dehydrogenase to a Long-Chain Amine Dehydrogenase by Mutagenesis of a Single Residue. Biochemistry, 2000, 39, 11184-11186.	2.5	25
128	Effects of Kinetic Coupling on Experimentally Determined Electron Transfer Parametersâ€. Biochemistry, 2000, 39, 4924-4928.	2.5	33
129	Amperometric Detection of Histamine with a Methylamine Dehydrogenase Polypyrrole-Based Sensor. Analytical Chemistry, 2000, 72, 2211-2215.	6.5	75
130	Molecular Basis for Complex Formation between Methylamine Dehydrogenase and Amicyanin Revealed by Inverse Mutagenesis of an Interprotein Salt Bridgeâ€. Biochemistry, 2000, 39, 8830-8836.	2.5	18
131	Characterization of the Tryptophan Tryptophyl-Semiquinone Catalytic Intermediate of Methylamine Dehydrogenase by Electron Spinâ^'Echo Envelope Modulation Spectroscopy. Journal of the American Chemical Society, 2000, 122, 931-938.	13.7	22
132	Tryptophan Tryptophylquinone Enzymes: Structure and Function. , 2000, , 197-202.		0
133	Heterologous Expression of Correctly Assembled Methylamine Dehydrogenase in Rhodobacter sphaeroides. Journal of Bacteriology, 1999, 181, 4216-4222.	2.2	58
134	Identification of a New Reaction Intermediate in the Oxidation of Methylamine Dehydrogenase by Amicyaninâ€. Biochemistry, 1999, 38, 4862-4867.	2.5	25
135	Gated and Ungated Electron Transfer Reactions from Aromatic Amine Dehydrogenase to Azurin. Journal of Biological Chemistry, 1999, 274, 29081-29086.	3.4	14
136	Methylamine Dehydrogenase: Structure and Function of Electron Transfer Complexes. Biochemical Society Transactions, 1999, 27, A30-A30.	3.4	0
137	Structure, Function, And Applications of Tryptophan Tryptophylquinone Enzymes. Advances in Experimental Medicine and Biology, 1999, 467, 587-595.	1.6	3
138	Localization of Periplasmic Redox Proteins of Alcaligenes faecalis by a Modified General Method for Fractionating Gram-Negative Bacteria. Journal of Bacteriology, 1999, 181, 6540-6542.	2.2	12
139	Methylamine dehydrogenase is a light-dependent oxidase. Biochimica Et Biophysica Acta - Bioenergetics, 1998, 1364, 297-300.	1.0	9
140	Electron Transfer from the Aminosemiquinone Reaction Intermediate of Methylamine Dehydrogenase to Amicyaninâ€. Biochemistry, 1998, 37, 11026-11032.	2.5	30
141	Site-Directed Mutagenesis of Phe 97 to Glu in Amicyanin Alters the Electronic Coupling for Interprotein Electron Transfer from Quinol Methylamine Dehydrogenaseâ€. Biochemistry, 1998, 37, 7371-7377.	2.5	28
142	Molecular Basis for Interprotein Complex-Dependent Effects on the Redox Properties of Amicyaninâ€. Biochemistry, 1998, 37, 17128-17136.	2.5	108
143	Refined crystal structure of methylamine dehydrogenase from Paracoccus denitrificans at 1.75 Ã... resolution. Journal of Molecular Biology, 1998, 276, 131-149.	4.2	106
144	Redox Properties of Tryptophan Tryptophylquinone Enzymes. Journal of Biological Chemistry, 1998, 273, 14254-14260.	3.4	22

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145	Catalytic Role of Monovalent Cations in the Mechanism of Proton Transfer Which Gates an Interprotein Electron Transfer Reaction. Biochemistry, 1997, 36, 13586-13592.	2.5	51
146	Factors Which Stabilize the Methylamine Dehydrogenaseâˆ'Amicyanin Electron Transfer Protein Complex Revealed by Site-Directed Mutagenesis. Biochemistry, 1997, 36, 12733-12738.	2.5	43
147	Kinetic Model for the Regulation by Substrate of Intramolecular Electron Transfer in Trimethylamine Dehydrogenaseâ€. Biochemistry, 1996, 35, 2445-2452.	2.5	15
148	Unraveling the Kinetic Complexity of Interprotein Electron Transfer Reactionsâ€. Biochemistry, 1996, 35, 14035-14039.	2.5	84
149	Electron Transfer from Copper to Heme within the Methylamine Dehydrogenaseâˆ'Amicyaninâˆ'Cytochromec-551i Complexâ€. Biochemistry, 1996, 35, 8120-8125.	2.5	51
150	Direct Detection by15N NMR of the Tryptophan Tryptophylquinone Aminoquinol Reaction Intermediate of Methylamine Dehydrogenase. Journal of the American Chemical Society, 1996, 118, 12868-12869.	13.7	34
151	Evidence for a Tryptophan Tryptophylquinone Aminosemiquinone Intermediate in the Physiologic Reaction between Methylamine Dehydrogenase and Amicyaninâ€. Biochemistry, 1996, 35, 8948-8954.	2.5	46
152	Intramolecular Electron Transfer in Trimethylamine Dehydrogenase:Â A Thermodynamic Analysisâ€. Biochemistry, 1996, 35, 12111-12118.	2.5	11
153	Enzymatic and Electron Transfer Activities in Crystalline Protein Complexes. Journal of Biological Chemistry, 1996, 271, 9177-9180.	3.4	53
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